

SEQUENCE LIST

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> EXPRESSION SYSTEMS OF TOXIC PROTEINS, VECTORS
AND PROCESS FOR MANUFACTURING TOXIC PROTEINS

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<150> FR N 02 11676

<151> 2002-09-20

<160> 53

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> PRT

<213> Hepatitis C virus

<400> 1

Met Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe
1 5 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe
20 25 30

Ala Gly Val Asp Ala
35

<210> 2

<211> 31

<212> PRT

<213> Hepatitis C virus

<400> 2

Met Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val
1 5 10 15

Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala
20 25 30

<210> 3

<211> 111

<212> DNA

<213> Hepatitis C virus

<400> 3

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<210> 4

<211> 93

<212> DNA

<213> Hepatitis C virus

<400> 4
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tggatgatgc tgctgatctc tcaggctgaa gct 93

<210> 5
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 5
gggaatgccca tatgatcgct ggtg 24

<210> 6
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 6
gcataatgat ctaagcgta aca 23

<210> 7
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: TME1 coding sens DNA
+ 3' cla I site

<400> 7
atgccatag atcgctggtg ctcaactggg tgttctggct ggtatcgctt acttctctat 60
ggttgtaac tgggctaaag ttctggtgt tctgctgctg ttcgctggtg ttgacgctta 120
gatcgatag c 131

<210> 8
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: anticodant sens DNA
+ 5' cla I site

<400> 8
gcataatgat ctaagcgta acaccagcga acagcagcag aacaaccaga acttagccc 60
agttaccaac catagagaag taagcgatac cagccagaac accccagtga gcaccagcga 120
tcatatggca t 131

<210> 9
<211> 74

<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
coding sens oligonucleotide for the synthesis of
TME1

<400> 9
atgccatatg atcgtctggg ctcactgggg tgtctggct ggtatcgctt acttctctat 60
ggttggaac tggg 74

<210> 10
<211> 79
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
anticoding sens oligonucleotide for the synthesis of
TME1

<400> 10
gcataatgat ctaagcgtca acaccagcga acagcagcag aacaaccaga acttagccc 60
agttaccaac catagagaa 79

<210> 11
<211> 22
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT without
the dp site

<400> 11
ggatccatgg aatacgttgt tc 22

<210> 12
<211> 28
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT with
the dp site

<400> 12
ggatccgacc cgatggaata cgtgttc 28

<210> 13
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:

oligonucleotide (-) of insertion into XKT

<400> 13
gaattcctaa gcttcagcct gag 23

<210> 14
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of transfert onto pET32a

<400> 14
gtgatatctg atctgtctgg tgggtgt 27

<210> 15
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 15
cgcatatgga cccgatcgct ggtgct 26

<210> 16
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 16
gaattcctaa gcgtcaacac cagc 24

<210> 17
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 17
catatggaat acgttggtc 19

<210> 18
<211> 28
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 18

aagcttaagc ttcagcctga gagatcag

28

<210> 19

<211> 103

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: sens DNA
coding TME2 + 5' Nde I site and 3' Hind III site

<400> 19

catatggaat acgtgttct gctgttctg ctgctggctg acgctcgtgt ttgctcttgc 60
ctgtggatga tgcgtctgat ctctcaggct gaagcttaag ctt 103

<210> 20

<211> 103

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: sens DNA
anticoding TME2 + 3' Nde I site and 5' Hind III site

<400> 20

aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagag caaacacgag 60
cgtcagccag cagcaggaac agcagaacaa cgtattccat atg 103

<210> 21

<211> 68

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
sens oligonucleotide (+) coding for the synthesis
of TME2

<400> 21

catatggaat acgtgttct gctgttctg ctgctggctg acgctcgtgt ttgctcttgc 60
ctgtggat 68

<210> 22

<211> 57

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
sens oligonucleotide (-) coding for the synthesis
of TME2

<400> 22

aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagac gaaacac 57

<210> 23
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT without
the dp site

<400> 23
ggatccgaat acgttggtc 19

<210> 24
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT with
the dp site

<400> 24
ggatccgacc cggaatacgt tggtc 25

<210> 25
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pGEXKT with
the dp site

<400> 25
gaattcttaa gcttcagcct gagagatcag 30

<210> 26
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 26
cgcatatgga cccggaatac gttgttc 27

<210> 27
<211> 27
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into p17-7

<400> 27

cagaattcct aagcttcagc ctgagag

27

<210> 28

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: end of the
GST followed by the thrombin site

<400> 28

Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly Ser

1 5 10 15

<210> 29

<211> 717

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA
coding for GST protein in the pGEXKT vector

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gatattgat acggtgttc gagaattgca tatagtaaag acttgaaac tctcaaagt 360
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tggccttg agggctggca agccacgtt ggtggtggcg accatcctcc aaaatcgat 660
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<210> 30

<211> 327

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA
coding for the thioredoxine in the pET32a+ vector

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gacggggcga tctcgtcga ttctgggca gagggtgctg gtccgtgcaa aatgatcgcc 120
ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttg aaaactgaac 180
atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgtg 240
ctgtcaaaa acggtgaagt ggcgggaacc aaagtgggtg cactgtctaa aggtcagttg 300
aaagattcc tcgacgctaa cctggcc 327

<210> 31
<211> 4969
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide
expressing pGEXKT

<400> 31

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<210> 32

<211> 11800

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide
expressing pET32a+

<400> 32

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<210> 33

<211> 2504

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide
expressing pT7-7

<400> 33

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 taactgtcag accaagtta ccatatata ctttagatt attt 2504

<210> 34

<211> 813

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
coding for fusion protein GST-DP-TME1

<400> 34

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 tggcgaaaca aaaagtgtg attgggttg gagtttcca atcttctta ttatattgat 180
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 gattttctta gcaagctacc tgaatgctg aaaatgtcg aagatcgtt atgtcataaa 420
 acatatttaa atgtgatca tgaacccat cctgacttca tgtgtatga cgctcttgat 480
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 ctgtctggtg gtggtggtgg tctggtccg cgtggatccg acccgatcgc tgggtctcac 720
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 gttgttctgc tctgttcgc tgggttgac gct 813

<210> 35

<211> 513

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
 coding for fusion protein TrX-DP-TME1

<400> 35

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 gacggggcga tctcgtcga ttctgggca gagtgggtgc gtccgtgcaa aatgatcgcc 120
 ccgattctgg atgaatcgc tgacgaatat cagggcaaac tgaccgttcg aaaactgaac 180
 atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
 ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
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 gtctgtgc tgttcgtggtg tgtgacgt tag 513

<210> 36

<211> 117

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
 coding for fusion protein M-DP-TME1

<400> 36

atggaccga tcgctggtgc tcactggggt gttctggctg gtatcgctta cttctctatg 60
 gttgtaact gggctaaagt tctggttgtt ctgctgctgt tcgctggtgt tgacgct 117

<210> 37

<211> 795

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
 coding for fusion protein
 GST-DP-TME2

<400> 37

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 ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa 120
 tggcgaaaca aaaagtgtga attgggtttg gagtttcca atcttcctta ttatattgat 180
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 tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat 660

ctgtctgggtg gtggtggtgg tctggttccg cgtg acccggaata cgtgttctg 720
ctgttctcgc tctggtcga cgctcgtgtt tctcttgc tgttgatgat gctgctgac 780
tctcaggctg aagct 795

<210> 38

<211> 486

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
coding for fusion protein
TrX-DP-TME2

<400> 38

atgagcgata aaattattca cctgactgac gacagtttg acacggatgt actcaaagcg 60
gacggggcga tctcgtcga tttctgggca gagtgggtgc gtccgtgcaa aatgatcgcc 120
ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgtgc aaaactgaac 180
atcgatcaaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
aaagagttcc tcgacgctaa cctggccggt tctggttctg gatctgatct gtctggtggt 360
gggtggtggtc tggttccgcg tggatccgac ccggaatacg ttgttctgct gttcctgctg 420
ctggtgacg ctcgtgttg ctcttcctg tggatgatgc tctgatctc tcaggctgaa 480
gcttag 486

<210> 39

<211> 99

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
coding for fusion protein M-DP-TME2

<400> 39

atggaccgg aatacgtgt tctgctgttc ctgctgctgg ctgacgctg tgttgcctc 60
tgcctgtgga tgatgctgt gatctctcag gctgaagct 99

<210> 40

<211> 5082

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pGEXKT-dp-Pt(TME1)

<400> 40

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tctggataat gtttttgcg ccgacatcat aacggttctg gcaaatattc tgaatgagc 180
tgttgacaat taatcatcgg ctcgtataat gtgtggaatt gtgagcggat aacaattca 240
cacaggaaac agtattcatg tcccctatac taggttattg gaaaattaag ggccttgtgc 300
aaccactcgc acttctttg gaatatctg aagaaaaata tgaagagcat ttgatgagc 360
gcgatgaagg tgataaatgg cgaaacaaaa agtttgaatt gggttggag ttcccaatc 420
ttccttatta tattgatgt gatgttaaat taacacagtc tatggccatc atacgtata 480
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tgtatgacgc tcttgatgtt gttttatata tggaccgcttgat gcgttcccaa 780
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 atcttccaaa atcggatctg tctggtggtg gtggtggtct ggtccgcgt ggatccgacc 960
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caggaaaggc agacgcgaat tatttttgat ggcgttgga tt 5082

<210> 41

<211> 5064

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pGEXKT-dp-Pt(TME2)

<400> 41

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tctggataat gtttttcgc ccgacatcat aacggttctg gcaaatattc tgaatgagc 180
tgttgacaat taatcatcgg ctctgataat gtgtggaatt gtgagcggat aacaatttca 240
cacaggaaac agtattcatg tcccctatac taggttattg gaaaattaag ggccttgtgc 300
aaccactcgc acttcttttg gaatatcttg aagaaaaata tgaagagcat ttgtatgagc 360
gcgatgaagg tgataaatgg cgaacaaaaa agtttgaatt gggtttgag ttcccaatc 420
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 attattttg atggcgttgg aatt 5064

<210> 42

<211> 5918

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pET32a-dp-Pt(TME1)

<400> 42

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 tgttagcagc cggatctcag tgggtgtgtt ggtgtgtctc gattgcggcc gcaagcttgt 180
 cgacggagct cgaattccta agcgtcaaca ccagcgaaca gcagcagaac aaccagaact 240
 ttgcccagt taccacaccat agagaagtaa gcgataccag ccagaacacc ccagtgcga 300
 ccagcgatcg ggtcggatcc acgcggaacc agaccaccac caccaccaga cagatccgat 360
 tttggagatc cagaaccaga accggccagg ttacgctga ggaactctt caactgacct 420

ttagacagt caccacttt ggttgccgc actt tttgaacag cagcagagtc 480
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 gcaacggta gtttccctg atattctca gcatctcat ccagaatcgg ggcgatcatt 600
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<210> 43

<211> 5891

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
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<400> 43

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 tgtagcagc cggatctcag tgggtgtgt ggtgtgtc gatgcggcc gcaagctgt 180
 cgacggagct cgaattccta agcttcagc tgagagatca gcagcatcat ccacaggcaa 240
 gagcaaacac gagcgtcagc cagcagcagg aacagcagaa caacgtattc cgggtcggat 300
 ccacgcggaa ccagaccacc accaccacca gacagatcag atccagaacc agaaccggcc 360
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 gccacttca cgttttgaa cagcagcaga gtcgggatac caggatgcc atattcggc 480
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 aggtgaataa tttatcgt catatgtata tctcttct aaagttaaac aaaattatt 720
 ctaggggga attgtatcc gtcacaatt cccctatagt gactgtatt aattcgcgg 780
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 cggtcacgt gcgcgtaacc accacaccg ccgcgctta tgcgccgta caggcgcggt 5880
 cccattcgcc a 5891

<210> 44

<211> 2617

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
 pT7-7-dp-Pt(TME1)

<400> 44

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 actttagccc agttaccaac catagagaag taagcgatac cagccagaac accccagtga 180
 gcaccagcga tcgggtccat atgtatatct cttcttaaa gtttaacaaa attatttcta 240
 gagggaaacc gttgtggtct ccctatagtg agtcgtatta attcgaagt ctatcagaag 300
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 cteccggaga cggtcacagc ttgtctgtaa gcggatgccg ggagcagaca agcccgtag 420
 ggcgcgtag cgggtgttgg cgggtgtcgg ggcgagcca tgaccagtc acgtagcgat 480
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 ccataggaag atcttcgga agatcttct atgcggtgtg aaataccgca cagatgcgta 600
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cagatggtaa gcctccctc atcgtagtta tctacacgac ggggagtcag gcaactatgg 2520
atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat tggtactgt 2580
cagaccaagt ttactcatat atactttaga ttgattt 2617

<210> 45

<211> 2599

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pT7-7-dp-Pt(TME2)

<400> 45

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caagagcaaa cacgagcgtc agccagcagc aggaacagca gaacaacgta ttccgggtcc 180
atatgtatat ctcttctta aagttaaaca aaattatttc tagagggaaa ccgttggtgt 240
ctccctatag tgagtctgat taatttcgaa gtctatcaga agttcgaatc gctgggcctc 300
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gaaagggcct cgtgatacgc ctattttat aggttaattg catgataata atggtttctt 1560
agacgtcagg tggcactttt cggggaaatg tgcgcggaac ccctatttgt ttattttct 1620
aaatacatc aaatatgtat ccgtcatga gacaataacc ctgataaatg cttaataat 1680
attgaaaaag gaagagtatg agtattcaac atttccgtgt cgccttatt ccctttttg 1740
cggcattttg ccttctgtt ttgtctacc cagaacgct ggtgaaagta aaagatgctg 1800
aagatcagtt ggtgcacga gtgggttaca tcgaactgga tctcaacagc ggtaagatcc 1860
ttgagagttt tcgccccgaa gaacgttttc caatgatgag cacttttaaa gttctgctat 1920
gtggcgcggt attatccgt gttagcggc ggcaagagca actcggctgc cgcatacact 1980
attctcagaa tgacttggtt gactactcac cagtcacaga aaagcatctt acggatggca 2040
tgacagtaag agaattatgc agtctgcca taaccatgag tgataaactc gcggccaact 2100
tacttctgac aacgatcgga ggaccgaagg agctaaccgc tttttgcac aacatggggg 2160
atcatgtaac tcgctttagt cgttgggaac cggagctgaa tgaagccata ccaaacgacg 2220
agcgtgacac cacgatgcct gtagcaatgg caacaacgtt gcgcaaaacta ttaactggcg 2280
aactacttac tctagcttcc cggaacaat taatagactg gatggaggcg gataaagttg 2340
caggaccact tctgcgctcg gcccttccgg ctggctggtt tattgctgat aaatctggag 2400
ccggtgagcg tgggtctcgc ggtatcattg cagcactggg gccagatggt aagccctccc 2460
gtatcgtagt tatctacacg acggggagtc aggcaactat ggatgaacga aatagacaga 2520
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<210> 46
<211> 271
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
GST-DP-TME1

<400> 46
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220
Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His
225 230 235 240
Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp
245 250 255
Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
260 265 270

<210> 47
<211> 265
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
GST-DP-TME2

<400> 47
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220
Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Glu Tyr Val Val Leu
225 230 235 240
Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met
245 250 255
Met Leu Leu Ile Ser Gln Ala Glu Ala
260 265

<210> 48
<211> 170
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
TrX-DP-TME1

<400> 48
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95
Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110
Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val
115 120 125
Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
130 135 140
Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145 150 155 160
Val Leu Leu Leu Phe Ala Gly Val Asp Ala
165 170

<210> 49
<211> 161
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
TrX-DP-TME2

<400> 49
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Leu Asn Ile Asp Gln Asn
50 55 60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110

Ser Gly Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly
115 120 125

Ser Asp Pro Glu Tyr Val Val Leu Phe Leu Leu Leu Ala Asp Ala
130 135 140

Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
145 150 155 160

Ala

<210> 50

<211> 39

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein
M-DP-TME1

<400> 50

Met Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala
1 5 10 15

Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu
20 25 30

Leu Phe Ala Gly Val Asp Ala
35

<210> 51

<211> 33

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein
M-DP-TME2

<400> 51

Met Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
1 5 10 15

Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
20 25 30

Ala

<210> 52
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
glutathion transferase (GST)

<400> 52
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220
Gly Gly Gly Leu Val Pro Arg Gly Ser Pro Gly Ile His Arg Asp
225 230 235

<210> 53
<211> 170
<212> PRT
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
thioredoxine (TrX)

<400> 53

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
50 55 60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110

Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val
115 120 125

Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
130 135 140

Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145 150 155 160

Val Leu Leu Leu Phe Ala Gly Val Asp Ala
165 170